Application No. 08/776,044

in a human patient having a neoplasia comprising:

- a) determining a nucleotide sequence of the <u>parts</u> [complete coding region] of a cander-related p53 protein <u>which encode</u> <u>biologically functional domains</u> from genomic DNA or cDNA derived from a human neoplastic tissue or body fluid;
- b) analyzing the nucleotide sequence determined in step a) for the presence of mutations; and
- c) classifying the neoplasia into different subgroups depending on
 - (i) the presence or absence of a mutation, and
 - (ii) whether the patient is node positive or not; and
- d) using the results of steps c) (i) and c (ii) in combination for prognosticating the development of the neoplasia and providing guidance for the treatment of the patient.
- 14. (Twice Amended) A method for prognostication of the development of neoplasia in a human patient having a neoplasia comprising:
- a) determining the nucleotide sequence of the <u>parts</u> [complete coding region] of a cancer-related p53 protein <u>which encode</u> biologically functional domains from genomic DNA or cDNA derived from a human neoplastic tissue or body fluid;

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- b) analyzing the nucle of tide sequence determined in step a) for the presence of mutations; and
- c) classifying the neoplasia into different subgroups depending on
 - (i) the presence or \absence of a mutation, and
 - (ii) whether the patient is node positive or not; and
- d) using the results of steps c)(i) and c(ii) in combination for prognosticating the development of the neoplasia.
- 15. (Twice Amended) A method for prognostication of the development of neoplasia in a human patient having a neoplasia comprising:
- a) determining the nucleotide sequence of the <u>parts</u> [complete coding region] of a cancer-related p53 protein <u>which encode</u> biologically functional domains from genomic DNA or cDNA derived from a human neoplastic tissue or body fluid;
- b) analyzing the entire nucleotide sequence determined in step

 a) for the presence of mutations; and
- c) classifying the neoplasia into different subgroups depending on the presence or absence of a mutation; and
- d) using the results of steps c) \underline{alone} for prognosticating the development of the neoplasia.